

March 10, 1964

Dear Luca--

I suppose you must be as busy as usual, but hope this will not keep from agreeing and making any necessary arrangements about coming over this summer with Alba and Matthew. Elliott was also hoping to hear from you concerning Matthew's interest in the physics program.

The polypeptide comparison programs have been working very well since just the time you were here -- and in general the computer work has been going very smoothly with the new people we have put on. But I think a very careful analysis of basic principles is needed, even more than the computation or mechanical statistical analysis. I am beginning to think that the structural requirements of the protein to function are overwhelmingly more important than mutational stability in the conservation (or rediscovery?) of sequences, and I really feel the need to discuss with you the ~~phylogenetic~~ significance of any such phylogenetic analyses. The resemblance of yeast cytochrome to human ~~cytochrome~~ cytochrome is staggering.

As you may see from some of the enclosed presentations, there is a good deal of internal regularity in the hemoglobin structures, undoubtedly related to their functional architecture. Also, the computer programs have brought attention to the 9-peptide string, 6-hydrophobic ~~residues~~ followed by III, which is common to the cytochromes and to myoglobin. This match is obtained by the correlation program under the "functional similarity" operator matrix. (However, I must say that a Monte Carlo randomization of the locations of the same amino acids gave as good a match in one of 20 trials).

We have the LINC under remote control operations too now, from my office and soon from the labs. But we have only a few useful programs so far.

Also included -- "Compact", to order a set of markers for mapping deletions. It can still be improved somewhat to produce a compact, consistent set of optimal size (by testing the effects of removing single rows from the consistent group on the admissibility to it of rows from the remainder.)

We are looking forward to your coming: there is still the problem of the minimum path of evolution from one string to another, and I think there may be another more suitable language for it ("SNOBOL" developed at Bell Labs). And there are many other things we want to be able to examine with you at more leisure than we could before. I am really glad we have the sm/suppressor story out now. What a ridiculous business with B and L.

The Interest check arrived some while ago, for which my thanks again. I hope you had a useful time at Midlands, or at least that you have made some happy arrangements by now.

As ever,